

BLAST Basic Local Alignment Search Tool

Edit and Resubmit Save Search Strategies Formatting options Download

Blast 2 sequences

seq id no:3 vs. McCaffrey no.1

Results for: **lcl|55517 None(206bp)**

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|55517

lcl|55517

Description

None

Molecule type

nucleic acid

Query Length

206

Subject ID

55519

Description

None

Molecule type

nucleic acid

Subject Length

25

Program

BLASTN 2.2.22+ Citation

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [Taxonomy reports](#)

Search Parameters

Program blastn
Word size 7
Expect value 10
Hitlist size 100
Match/Mismatch scores 2,-3
Gapcosts 5,2
Low Complexity Filter Yes
Filter string L,m;
Genetic Code 1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

Effective search space 3582

[Graphic Summary](#)

Distribution of Blast Hits on the Query Sequence



An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

seq id no:3 vs. McCaffrey no.2

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|28559

lcl|28559

Description

None

Molecule type

nucleic acid

Query Length

206

Subject ID

28561

Description

None

Molecule type

nucleic acid

Subject Length

25

Program

BLASTN 2.2.22+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons [why](#), [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

Search Parameters

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L,m;
Genetic Code	1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

Effective search space 3582

[Graphic Summary](#)

Distribution of Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

BLAST Basic Local Alignment Search Tool

EXHIBIT

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Blast 2 sequences

seq id no:3 vs. McCaffrey no 3

Results for: lcl|61181 None(206bp)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|61181

lcl|61181

Description

None

Molecule type

nucleic acid

Query Length

206

Subject ID

61183

Description

None

Molecule type

nucleic acid

Subject Length

25

Program

BLASTN 2.2.22+ Citation

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.
Other reports: [Search Summary](#) [[Taxonomy reports](#)]

Search Parameters

Program	blastn
Word size	7
Expect value	10
Hittlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L,m;
Genetic Code	1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

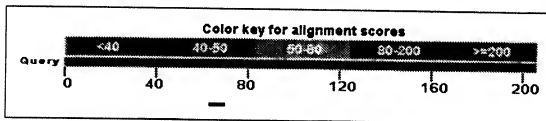
Effective search space 3582

Graphic Summary

Distribution of 1 Blast Hits on the Query Sequence

?

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



[Dot Matrix View](#) ✓**Plot of lcl|61181 vs 61183 [?]**

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

**Descriptions**

Legend for links to other resources: **U** UniGene **E** GEO **G** Gene **S** Structure **M** Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

61183	13.9	13.9	3%	0.23	100%
-------	------	------	----	------	------

[Alignments](#) [Select All](#) [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#) 

>lcl|61183


Length=25

Score = 13.9 bits (14), Expect = 0.23
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Plus

Query 65 GCCAAGT 71

|||||||

Sbjct 18 GCCAAGT 24

[Select All](#) [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#) 

BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

seq id no:3 vs. McCaffrey no 4

Results for: "lcl|4723 None(206bp)"

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|4723

lcl|4723

Description

None

Molecule type

nucleic acid

Query Length

206

Subject ID

4725

Description

None

Molecule type

nucleic acid

Subject Length

25

Program

BLASTN 2.2.22+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

Search Parameters

Program	blastn
Word size	7
Expect value	10
Hittlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L,m;
Genetic Code	1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408148	0.41
H	0.912438	0.78

Results Statistics

Effective search space 3582

Graphic Summary

Distribution of Blast Hits on the Query Sequence



An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

seq id no:3 vs. McCaffrey no 4

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|4723

lcl|4723

Description

None

Molecule type

nucleic acid

Query Length

206

Subject ID

4725

Description

None

Molecule type

nucleic acid

Subject Length

25

Program

BLASTN 2.2.22+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [\[Taxonomy reports\]](#)

Search Parameters

Program blastn
Word size 7
Expect value 10
Hitlist size 100
Match/Mismatch scores 2,-3
Gapcosts 5,2
Low Complexity Filter Yes
Filter string L;m;
Genetic Code 1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

Effective search space 3582

Graphic Summary

Distribution of Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

seq id no:3 vs. McCaffrey no 5

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|21471

lcl|21471

Description

None

Molecule type

nucleic acid

Query Length

206

Subject ID

21473

Description

None

Molecule type

nucleic acid

Subject Length

25

Program

BLASTN 2.2.22+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

Search Parameters

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

Effective search space 3582

[Graphic Summary](#)

Distribution of Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

seq id no:3 vs. McCaffrey no 6

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|31433

lcl|31433

Description

None

Molecule type

nucleic acid

Query Length

206

Subject ID

31435

Description

None

Molecule type

nucleic acid

Subject Length

25

Program

BLASTN 2.2.22+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

Search Parameters

Program	blastn
Word size	7
Expect value	10
Hittlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L,m;
Genetic Code	1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

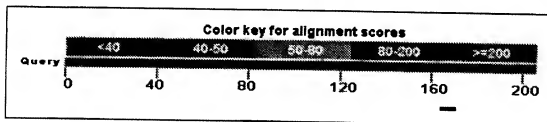
Effective search space 3582

Graphic Summary

Distribution of 1 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



[Dot Matrix View](#) **Plot of lcl|31433 vs 31435 [?]**

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

**Descriptions**

Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

31435	13.9	13.9	3%	0.23	100%
-------	------	------	----	------	------

[Alignments](#) [Select All](#) [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#) [Help](#)

>lc1131435

Length=25

Score = 13.9 bits (14), Expect = 0.23
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Plus

Query 166 GAACTCC 172

Sbjct 11 GAACTCC 17

[Select All](#) [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#) [Help](#)

BLAST Basic Local Alignment Search Tool

EXHIBIT 1

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Blast 2 sequences

seq id no:3 vs. McCaffrey no 7

Results for: **"|c|38455 None(206bp)"**

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

|c|38455

|c|38455

Description

None

Molecule type

nucleic acid

Query Length

206

Subject ID

38457

Description

None

Molecule type

nucleic acid

Subject Length

25

ProgramBLASTN 2.2.22+ [Citation](#)**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons [why](#), [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

Search Parameters

Program	blastn
Word size	7
Expect value	10
Hittist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

Effective search space 3582

[Graphic Summary](#)

Distribution of Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

SEQ ID NO. 10 vs. McCAFFREY NO.1

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

Ic|45183

Ic|45183

Description

None

Molecule type

nucleic acid

Query Length

71

Subject ID

45185

Description

None

Molecule type

nucleic acid

Subject Length

25

Program

BLASTN 2.2.22+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

Search Parameters

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L,m;
Genetic Code	1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

Effective search space 1320

[Graphic Summary](#)

Distribution of Blast Hits on the Query Sequence



An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

SEQ ID NO. 10 vs. McCaffrey NO.2

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|53051

lcl|53051

Description

None

Molecule type

nucleic acid

Query Length

71

Subject ID

53053

Description

None

Molecule type

nucleic acid

Subject Length

25

Program

BLASTN 2.2.22+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

Search Parameters

Program blastn
Word size 7
Expect value 10
Hitlist size 100
Match/Mismatch scores 2,-3
Gapcosts 5,2
Low Complexity Filter Yes
Filter string L,m;
Genetic Code 1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

Effective search space 1320

[Graphic Summary](#)

Distribution of Blast Hits on the Query Sequence

[?]


An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

SEQ ID NO. 10 vs. McCAFFREY NO.3

Results for: 

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

|cl|3921

|cl|3921

Description

None

Molecule type

nucleic acid

Query Length

71

Subject ID

3923

Description

None

Molecule type

nucleic acid

Subject Length

25

Program

BLASTN 2.2.22+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

Search Parameters

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L,m;
Genetic Code	1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

Effective search space 1320

[Graphic Summary](#)

Distribution of Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

SEQ ID NO. 10 vs. McCAFFREY NO.4

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

ic|59547

ic|59547

Description

None

Molecule type

nucleic acid

Query Length

71

Subject ID

59549

Description

None

Molecule type

nucleic acid

Subject Length

25

Program

BLASTN 2.2.22+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [Taxonomy reports](#)

Search Parameters

Program	blastn
Word size	7
Expect value	10
Hittist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L,m;
Genetic Code	1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408148	0.41
H	0.912438	0.78

Results Statistics

Effective search space 1320

[Graphic Summary](#)

Distribution of Blast Hits on the Query Sequence



An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

BLAST Basic Local Alignment Search Tool

•
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Blast 2 sequences

SEQ ID NO. 10 vs. McCaffrey NO.5

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|10651

lcl|10651

Description

None

Molecule type

nucleic acid

Query Length

71

Subject ID

10653

Description

None

Molecule type

nucleic acid

Subject Length

25

Program

BLASTN 2.2.22+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [Taxonomy reports](#)

Search Parameters

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L,m;
Genetic Code	1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

Effective search space 1320

[Graphic Summary](#)

Distribution of Blast Hits on the Query Sequence



An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

SEQ ID NO. 10 vs. McCAFFREY NO.6

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

ici|26449

ici|26449

Description

None

Molecule type

nucleic acid

Query Length

71

Subject ID

26451

Description

None

Molecule type

nucleic acid

Subject Length

25

Program

BLASTN 2.2.22+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

Search Parameters

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

Effective search space 1320

[Graphic Summary](#)

Distribution of Blast Hits on the Query Sequence

[?]


An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

SEQ ID NO. 10 vs. McCAFFREY NO.7

Results for: 

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

|c|32359

|c|32359

Description

None

Molecule type

nucleic acid

Query Length

71

Subject ID

32361

Description

None

Molecule type

nucleic acid

Subject Length

25

Program

BLASTN 2.2.22+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons [why, click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

Search Parameters

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L,m;
Genetic Code	1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

Effective search space 1320

[Graphic Summary](#)

Distribution of Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.